

<110> SunGene GmbH & Co.KGaA

<120> DNA-Sequenz kodierend fuer eine
1-Deoxy-D-xylulose-5-phosphat Synthase

<130> 0050/49249

<140> 0817 - 00006

<141> 1999-08-04

<160> 8

<170> PatentIn Vers. 2.0

<210> 1

<211> 2458

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2154)

<400> 1

| | |
|-----------------------------------------------------------------|----|
| atg gct tct tct gca ttt gct ttt cct tct tac ata ata acc aaa gga | 48 |
| Met Ala Ser Ser Ala Phe Ala Phe Pro Ser Tyr Ile Ile Thr Lys Gly | |
| 1 5 10 15 | |

| | |
|-----------------------------------------------------------------|----|
| gga ctt tca act gat tct tgt aaa tca act tct ttg tct tct tct aga | 96 |
| Gly Leu Ser Thr Asp Ser Cys Lys Ser Thr Ser Leu Ser Ser Ser Arg | |
| 20 25 30 | |

| | |
|-----------------------------------------------------------------|-----|
| tct ttg gtt aca gat ctt cca tca cca tgt ctg aaa ccc aac aac aat | 144 |
| Ser Leu Val Thr Asp Leu Pro Ser Pro Cys Leu Lys Pro Asn Asn Asn | |
| 35 40 45 | |

| | |
|-----------------------------------------------------------------|-----|
| tcc cat tca aac aga aga gca aaa gtg tgt gct tca ctt gca gag aag | 192 |
| Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys | |
| 50 55 60 | |

| | |
|-----------------------------------------------------------------|-----|
| ggt gaa tat tat tca aac aga cca cca act cca tta ctt gac act att | 240 |
| Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile | |
| 65 70 75 80 | |

| | |
|-----------------------------------------------------------------|-----|
| aac tac cca atc cac atg aaa aat ctt tct gtc aag gaa ctg aaa caa | 288 |
| Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln | |

85

90

95

ctt tct gat gag ctg aga tca gac gtg atc ttt aat gtg tcg aaa acc 336
 Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr
 100 105 110

ggg gga cat ttg ggg tca agt ctt ggt gtt gtg gag ctt act gtg gct 384
 Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala
 115 120 125

ctt cat tac att ttc aat act cca caa gac aag att ctt tgg gat gtt 432
 Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val
 130 135 140

ggg cat cag tct tat cct cat aag att ctt act ggg aga aga gga aag 480
 Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys
 145 150 155 160

atg cct aca atg agg caa acc aat ggt ctc tct ggt ttc acc aaa cga 528
 Met Pro Thr Met Arg Gln Thr Asn Gly Leu Ser Gly Phe Thr Lys Arg
 165 170 175

gga gag agt gaa cat gat tgc ttt ggt act gga cac agc tca acc aca 576
 Gly Glu Ser Glu His Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr
 180 185 190

ata tct gct ggt tta gga atg gcg gta gga agg gat ttg aag ggg aag 624
 Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys
 195 200 205

aac aac aat gtg gtt gct gtg att ggt gat ggt gcg atg acg gca gga 672
 Asn Asn Asn Val Val Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly
 210 215 220

cag gct tat gaa gcc atg aac aac gcc gga tat cta gac tct gat atg 720
 Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met
 225 230 235 240

att gtg att ctt aat gac aac aag caa gtc tca tta cct aca gct act 768
 Ile Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Thr
 245 250 255

ttg gat gga cca agt cca cct gtt ggt gca ttg agc agt gct ctt agt 816
 Leu Asp Gly Pro Ser Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser
 260 265 270

cgg tta cag tct aac ccg gct ctc aga gag ttg aga gaa gtc gca aag 864
 Arg Leu Gln Ser Asn Pro Ala Leu Arg Glu Leu Arg Glu Val Ala Lys

| 275 | 280 | 285 | |
|-----------------------------------------------------------------|-----|-----|------|
| ggt atg aca aag caa ata ggc gga cca atg cat cag ttg gcg gct aag | | | 912 |
| Gly Met Thr Lys Gln Ile Gly Gly Pro Met His Gln Leu Ala Ala Lys | | | |
| 290 | 295 | 300 | |
| gta gat gtg tat gct cga gga atg ata agc ggt act gga tcg tca ctg | | | 960 |
| Val Asp Val Tyr Ala Arg Gly Met Ile Ser Gly Thr Gly Ser Ser Leu | | | |
| 305 | 310 | 315 | 320 |
| ttt gaa gaa ctc ggt ctt tac tat att ggt cca gtt gat ggg cac aac | | | 1008 |
| Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn | | | |
| 325 | 330 | 335 | |
| ata gat gat ttg gta gcc att ctt aaa gaa gtt aag agt acc aga acc | | | 1056 |
| Ile Asp Asp Leu Val Ala Ile Leu Lys Glu Val Lys Ser Thr Arg Thr | | | |
| 340 | 345 | 350 | |
| aca gga cct gta ctt att cat gtg gtg acg gag aaa ggt cgt ggt tat | | | 1104 |
| Thr Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr | | | |
| 355 | 360 | 365 | |
| cct tac gcg gag aga gct gat gac aaa tac cat ggt gtt gtg aaa ttt | | | 1152 |
| Pro Tyr Ala Glu Arg Ala Asp Asp Lys Tyr His Gly Val Val Lys Phe | | | |
| 370 | 375 | 380 | |
| gat cca gca acg ggt aga cag ttc aaa act act aat gag act caa tct | | | 1200 |
| Asp Pro Ala Thr Gly Arg Gln Phe Lys Thr Thr Asn Glu Thr Gln Ser | | | |
| 385 | 390 | 395 | 400 |
| tac aca act tac ttt gcg gag gca tta gtc gca gaa gca gag gta gac | | | 1248 |
| Tyr Thr Thr Tyr Phe Ala Glu Ala Leu Val Ala Glu Ala Glu Val Asp | | | |
| 405 | 410 | 415 | |
| aaa gat gtg gtt gcg att cat gca gcc atg gga ggt gga acc ggg tta | | | 1296 |
| Lys Asp Val Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Leu | | | |
| 420 | 425 | 430 | |
| aat ctc ttt caa cgt cgc ttc cca aca aga tgt ttc gat gta gga ata | | | 1344 |
| Asn Leu Phe Gln Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile | | | |
| 435 | 440 | 445 | |
| gcg gaa caa cac gca gtt act ttt gct gcg ggt tta gcc tgt gaa ggc | | | 1392 |
| Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly | | | |
| 450 | 455 | 460 | |
| ctt aaa ccc ttc tgt gca atc tat tcg tct ttc atg cag cgt gct tat | | | 1440 |
| Leu Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr | | | |

| 465 | 470 | 475 | 480 | |
|-----------------------------------------------------------------|-----|-----|-----|------|
| gac cag gtt gtc cat gat gtt gat ttg caa aaa tta ccg gtg aga ttt | | | | 1488 |
| Asp Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe | | | | |
| | 485 | 490 | 495 | |
| gca atg gat aga gct gga ctc gtt gga gct gat ggt ccg aca cat tgt | | | | 1536 |
| Ala Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys | | | | |
| | 500 | 505 | 510 | |
| gga gct ttc gat gtg aca ttt atg gct tgt ctt cct aac atg ata gtg | | | | 1584 |
| Gly Ala Phe Asp Val Thr Phe Met Ala Cys Leu Pro Asn Met Ile Val | | | | |
| | 515 | 520 | 525 | |
| atg gct cca tca gat gaa gca gat ctc ttt aac atg gtt gca act gct | | | | 1632 |
| Met Ala Pro Ser Asp Glu Ala Asp Leu Phe Asn Met Val Ala Thr Ala | | | | |
| | 530 | 535 | 540 | |
| gtt gcg att gat gat cgt cct tct tgt ttc cgt tac cct aga ggt aac | | | | 1680 |
| Val Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn | | | | |
| | 545 | 550 | 555 | 560 |
| ggt att gga gtt gca tta cct ccc gga aac aaa ggt gtt cca att gag | | | | 1728 |
| Gly Ile Gly Val Ala Leu Pro Pro Gly Asn Lys Gly Val Pro Ile Glu | | | | |
| | 565 | 570 | 575 | |
| att ggg aaa ggt aga att tta aag gaa gga gag aga gtt gcg ttg ttg | | | | 1776 |
| Ile Gly Lys Gly Arg Ile Leu Lys Glu Gly Glu Arg Val Ala Leu Leu | | | | |
| | 580 | 585 | 590 | |
| ggt tat ggc tca gca gtt cag agc tgt tta gga gcg gct gta atg ctc | | | | 1824 |
| Gly Tyr Gly Ser Ala Val Gln Ser Cys Leu Gly Ala Ala Val Met Leu | | | | |
| | 595 | 600 | 605 | |
| gaa gaa cgc gga tta aac gta act gta gcg gat gca cgg ttt tgc aag | | | | 1872 |
| Glu Glu Arg Gly Leu Asn Val Thr Val Ala Asp Ala Arg Phe Cys Lys | | | | |
| | 610 | 615 | 620 | |
| cca ttg gac cgt gct ctc att cgc agc tta gct aag tcg cac gag gtt | | | | 1920 |
| Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val | | | | |
| | 625 | 630 | 635 | 640 |
| ctg atc acg gtt gaa gaa ggt tcc att gga ggt ttt ggc tcg cac gtt | | | | 1968 |
| Leu Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val | | | | |
| | 645 | 650 | 655 | |
| gtt cag ttt ctt gct ctc gat ggt ctt ctt gat ggc aaa ctc aag tgg | | | | 2016 |
| Val Gln Phe Leu Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp | | | | |

660

665

670

aga cca atg gta ctg cct gat cga tac att gat cac ggt gca cca gct 2064
 Arg Pro Met Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ala Pro Ala
 675 680 685

gat caa cta gct gaa gct gga ctc atg cca tct cac atc gca gca acc 2112
 Asp Gln Leu Ala Glu Ala Gly Leu Met Pro Ser His Ile Ala Ala Thr
 690 695 700

gca ctt aac tta atc ggt gca cca agg gaa gct ctg ttt tga 2154
 Ala Leu Asn Leu Ile Gly Ala Pro Arg Glu Ala Leu Phe
 705 710 715

gagtaagaat ctgttggtta aaacatatgt atacaaacac tctaaatgca acccaagggtt 2214

tcttctaagt actgatcaga attcccgccc gagaagtcct ttggcaacag ctatatatat 2274

ttactaagat tgtgaagaga aaggcaaagg caaagggttg gcaaagatta gtattataga 2334

taaaactggt atttggtttg taattttagg attgtgatga gatcgtgttg taccaataac 2394

taacatcttg taaaatcaat tactctcttg tgatcttcaa taagcttgag tgacaaaaaa 2454

aaaa 2458

<210> 2

<211> 717

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Ala Ser Ser Ala Phe Ala Phe Pro Ser Tyr Ile Ile Thr Lys Gly
 1 5 10 15

Gly Leu Ser Thr Asp Ser Cys Lys Ser Thr Ser Leu Ser Ser Ser Arg
 20 25 30

Ser Leu Val Thr Asp Leu Pro Ser Pro Cys Leu Lys Pro Asn Asn Asn
 35 40 45

Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys
 50 55 60

Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile
 65 70 75 80

Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln
85 90 95

Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr
100 105 110

Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala
115 120 125

Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val
130 135 140

Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys
145 150 155 160

Met Pro Thr Met Arg Gln Thr Asn Gly Leu Ser Gly Phe Thr Lys Arg
165 170 175

Gly Glu Ser Glu His Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr
180 185 190

Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys
195 200 205

Asn Asn Asn Val Val Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly
210 215 220

Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met
225 230 235 240

Ile Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Thr
245 250 255

Leu Asp Gly Pro Ser Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser
260 265 270

Arg Leu Gln Ser Asn Pro Ala Leu Arg Glu Leu Arg Glu Val Ala Lys
275 280 285

Gly Met Thr Lys Gln Ile Gly Gly Pro Met His Gln Leu Ala Ala Lys
290 295 300

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Val | Tyr | Ala | Arg | Gly | Met | Ile | Ser | Gly | Thr | Gly | Ser | Ser | Leu |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |

Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn
325 330 335

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|-----|
| Ile Asp Asp | Leu Val Ala | Ile Leu Lys | Glu Val Lys | Ser Thr Arg | Thr |
| 340 | | 345 | | 350 | |
| Thr Gly Pro | Val Leu Ile | His Val Val | Thr Glu Lys | Gly Arg Gly | Tyr |
| 355 | | 360 | | 365 | |
| Pro Tyr Ala | Glu Arg Ala | Asp Asp Lys | Tyr His Gly | Val Val Lys | Phe |
| 370 | | 375 | | 380 | |
| Asp Pro Ala | Thr Gly Arg | Gln Phe Lys | Thr Thr Asn | Glu Thr Gln | Ser |
| 385 | | 390 | | 395 | 400 |
| Tyr Thr Thr | Tyr Phe Ala | Glu Ala Leu | Val Ala Glu | Ala Glu Val | Asp |
| | 405 | | 410 | | 415 |
| Lys Asp Val | Val Ala Ile | His Ala Ala | Met Gly Gly | Gly Thr Gly | Leu |
| | 420 | | 425 | | 430 |
| Asn Leu Phe | Gln Arg Arg | Phe Pro Thr | Arg Cys Phe | Asp Val Gly | Ile |
| | 435 | | 440 | | 445 |
| Ala Glu Gln | His Ala Val | Thr Phe Ala | Ala Gly Leu | Ala Cys Glu | Gly |
| | 450 | | 455 | | 460 |
| Leu Lys Pro | Phe Cys Ala | Ile Tyr Ser | Ser Phe Met | Gln Arg Ala | Tyr |
| 465 | | 470 | | 475 | 480 |
| Asp Gln Val | Val His Asp | Val Asp Leu | Gln Lys Leu | Pro Val Arg | Phe |
| | 485 | | 490 | | 495 |
| Ala Met Asp | Arg Ala Gly | Leu Val Gly | Ala Asp Gly | Pro Thr His | Cys |
| | 500 | | 505 | | 510 |
| Gly Ala Phe | Asp Val Thr | Phe Met Ala | Cys Leu Pro | Asn Met Ile | Val |
| | 515 | | 520 | | 525 |
| Met Ala Pro | Ser Asp Glu | Ala Asp Leu | Phe Asn Met | Val Ala Thr | Ala |
| | 530 | | 535 | | 540 |
| Val Ala Ile | Asp Asp Arg | Pro Ser Cys | Phe Arg Tyr | Pro Arg Gly | Asn |
| 545 | | 550 | | 555 | 560 |
| Gly Ile Gly | Val Ala Leu | Pro Pro Gly | Asn Lys Gly | Val Pro Ile | Glu |
| | 565 | | 570 | | 575 |
| Ile Gly Lys | Gly Arg Ile | Leu Lys Glu | Gly Glu Arg | Val Ala Leu | Leu |
| | 580 | | 585 | | 590 |

Gly Tyr Gly Ser Ala Val Gln Ser Cys Leu Gly Ala Ala Val Met Leu
595 600 605

Glu Glu Arg Gly Leu Asn Val Thr Val Ala Asp Ala Arg Phe Cys Lys
610 615 620

Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val
625 630 635 640

Leu Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val
645 650 655

Val Gln Phe Leu Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp
660 665 670

Arg Pro Met Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ala Pro Ala
675 680 685

Asp Gln Leu Ala Glu Ala Gly Leu Met Pro Ser His Ile Ala Ala Thr
690 695 700

Ala Leu Asn Leu Ile Gly Ala Pro Arg Glu Ala Leu Phe
705 710 715

<210> 3

<211> 1863

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1863)

<400> 3

atg agt ttt gat att gcc aaa tac ccg acc ctg gca ctg gtc gac tcc 48
Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
1 5 10 15

acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc 96
Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
20 25 30

gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg 144
Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
35 40 45

cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac 192

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
 50 55 60

tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat 240
 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
 65 70 75 80

cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc 288
 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
 85 90 95

acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa 336
 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
 100 105 110

agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt 384
 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
 115 120 125

gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc 432
 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
 130 135 140

cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg 480
 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
 145 150 155 160

ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg 528
 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
 165 170 175

att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc 576
 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
 180 185 190

aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg 624
 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
 195 200 205

cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag 672
 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
 210 215 220

ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc 720
 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
 225 230 235 240

acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccg gtg gac ggt 768

| Thr | Leu | Phe | Glu | Glu | Leu | Gly | Phe | Asn | Tyr | Ile | Gly | Pro | Val | Asp | Gly | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----------------------------------------------------|-----|-----|-----|-----|-----|------|--|--|
| | | | 245 | | | | | | 250 | | | | | | 255 | | | |
| cac | gat | gtg | ctg | ggg | ctt | atc | acc | acg | cta | aag | aac | atg | cgc | gac | ctg | 816 | | |
| His | Asp | Val | Leu | Gly | Leu | Ile | Thr | Thr | Leu | Lys | Asn | Met | Arg | Asp | Leu | | | |
| | | | 260 | | | | | | 265 | | | | | | 270 | | | |
| aaa | ggc | ccg | cag | ttc | ctg | cat | atc | atg | acc | aaa | aaa | ggt | cgt | ggt | tat | 864 | | |
| Lys | Gly | Pro | Gln | Phe | Leu | His | Ile | Met | Thr | Lys | Lys | Gly | Arg | Gly | Tyr | | | |
| | | | 275 | | | | | | 280 | | | | | | 285 | | | |
| gaa | ccg | gca | gaa | aaa | gac | ccg | atc | act | ttc | cac | gcc | gtg | cct | aaa | ttt | 912 | | |
| Glu | Pro | Ala | Glu | Lys | Asp | Pro | Ile | Thr | Phe | His | Ala | Val | Pro | Lys | Phe | | | |
| | | | 290 | | | | | | 295 | | | | | | 300 | | | |
| gat | ccc | tcc | agc | ggt | tgt | ttg | ccg | aaa | agt | agc | ggc | ggt | ttg | ccg | agc | 960 | | |
| Asp | Pro | Ser | Ser | Gly | Cys | Leu | Pro | Lys | Ser | Ser | Gly | Gly | Leu | Pro | Ser | | | |
| 305 | | | | 310 | | | | | | 315 <td colspan="3"></td> <th colspan="3">320</th> | | | | | | 320 | | |
| tat | tca | aaa | atc | ttt | ggc | gac | tgg | ttg | tgc | gaa | acg | gca | gcg | aaa | gac | 1008 | | |
| Tyr | Ser | Lys | Ile | Phe | Gly | Asp | Trp | Leu | Cys | Glu | Thr | Ala | Ala | Lys | Asp | | | |
| | | | 325 | | | | | | 330 | | | | | | 335 | | | |
| aac | aag | ctg | atg | gcg | att | act | ccg | gcg | atg | cgt | gaa | ggt | tcc | ggc | atg | 1056 | | |
| Asn | Lys | Leu | Met | Ala | Ile | Thr | Pro | Ala | Met | Arg | Glu | Gly | Ser | Gly | Met | | | |
| | | | 340 | | | | | | 345 | | | | | | 350 | | | |
| gtc | gag | ttt | tca | cgt | aaa | ttc | ccg | gat | cgc | tac | ttc | gac | gtg | gca | att | 1104 | | |
| Val | Glu | Phe | Ser | Arg | Lys | Phe | Pro | Asp | Arg | Tyr | Phe | Asp | Val | Ala | Ile | | | |
| | | | 355 | | | | | | 360 | | | | | | 365 | | | |
| gcc | gag | caa | cac | gcg | gtg | acc | ttt | gct | gcg | ggt | ctg | gcg | att | ggt | ggg | 1152 | | |
| Ala | Glu | Gln | His | Ala | Val | Thr | Phe | Ala | Ala | Gly | Leu | Ala | Ile | Gly | Gly | | | |
| | | | 370 | | | | | | 375 | | | | | | 380 | | | |
| tac | aaa | ccc | att | gtc | gcg | att | tac | tcc | act | ttc | ctg | caa | cgc | gcc | tat | 1200 | | |
| Tyr | Lys | Pro | Ile | Val | Ala | Ile | Tyr | Ser | Thr | Phe | Leu | Gln | Arg | Ala | Tyr | | | |
| 385 | | | | 390 | | | | | | 395 | | | | | | 400 | | |
| gat | cag | gtg | ctg | cat | gac | gtg | gcg | att | caa | aag | ctt | ccg | gtc | ctg | ttc | 1248 | | |
| Asp | Gln | Val | Leu | His | Asp | Val | Ala | Ile | Gln | Lys | Leu | Pro | Val | Leu | Phe | | | |
| | | | 405 | | | | | | 410 | | | | | | 415 | | | |
| gcc | atc | gac | cgc | gcg | ggc | att | gtt | ggt | gct | gac | ggt | caa | acc | cat | cag | 1296 | | |
| Ala | Ile | Asp | Arg | Ala | Gly | Ile | Val | Gly | Ala | Asp | Gly | Gln | Thr | His | Gln | | | |
| | | | 420 | | | | | | 425 | | | | | | 430 | | | |
| ggt | gct | ttt | gat | ctc | tct | tac | ctg | cgc | tgc | ata | ccg | gaa | atg | gtc | att | 1344 | | |

| | |
|-----------------------------------------------------------------|-----------------|
| Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile | |
| 435 | 440 445 |
| atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc | 1392 |
| Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly | |
| 450 | 455 460 |
| tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac | 1440 |
| Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn | |
| 465 | 470 475 480 |
| gcg gtc ggc gtg gaa ctg acg ccg ctg gaa aaa cta cca att ggc aaa | 1488 |
| Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys | |
| | 485 490 495 |
| ggc att gtg aag cgt cgt ggc gag aaa ctg gcg atc ctt aac ttt ggt | 1536 |
| Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly | |
| | 500 505 510 |
| acg ctg atg cca gaa gcg gcg aaa gtc gcc gaa tcg ctg aac gcc acg | 1584 |
| Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr | |
| | 515 520 525 |
| ctg gtc gat atg cgt ttt gtg aaa ccg ctt gat gaa gcg tta att ctg | 1632 |
| Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu | |
| | 530 535 540 |
| gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc | 1680 |
| Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala | |
| | 545 550 555 560 |
| att atg ggc ggc gca ggc agc ggc gtg aac gaa gtg ctg atg gcc cat | 1728 |
| Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His | |
| | 565 570 575 |
| cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att | 1776 |
| Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile | |
| | 580 585 590 |
| ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc | 1824 |
| Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala | |
| | 595 600 605 |
| gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca taa | 1863 |
| Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala | |
| | 610 615 620 |

<210> 4

<211> 620

<212> PRT

<213> Escherichia coli

<400> 4

Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
 1 5 10 15

Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
 20 25 30

Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
 35 40 45

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
 50 55 60

Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
 65 70 75 80

Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
 85 90 95

Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
 100 105 110

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
 115 120 125

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
 130 135 140

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
 145 150 155 160

Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
 165 170 175

Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
 180 185 190

Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
 195 200 205

Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
 210 215 220

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
 225 230 235 240

Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
 245 250 255

His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
 260 265 270

Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
 275 280 285

Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
 290 295 300

Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
 305 310 315 320

Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
 325 330 335

Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
 340 345 350

Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
 355 360 365

Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
 370 375 380

Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
 385 390 395 400

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
 405 410 415

Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
 420 425 430

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
 435 440 445

Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
 450 455 460

Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
 465 470 475 480

Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
 485 490 495

Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
 500 505 510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
 515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
 530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
 545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
 565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
 580 585 590

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
 595 600 605

Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
 610 615 620

<210> 5

<211> 1469

<212> DNA

<213> *Streptomyces avermitilis*

<220>

<221> CDS

<222> (218) .. (1138)

<400> 5

gatatccgag cgccgcccggg tccactgctg tccgaagccg cggatgactc cattcgactg 60

aagccgggtcg agccgcgcct gcacgggtgcc gcgcgcgacc ccgagccgcc gggacatctc 120

gagcactccg atgcgcggct cccgcgccag cagcaccagg agccggccgt ccagatgata 180

gatcgccacg gcagcccctc cagtggatcat cctgtac atg cag ccc cac gcc atg 235

Met Gln Pro His Ala Met

1

5

| | |
|-----------------------------------------------------------------|-----|
| ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca | 283 |
| Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala | |
| 10 15 20 | |
| cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca | 331 |
| Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro | |
| 25 30 35 | |
| cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat | 379 |
| His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn | |
| 40 45 50 | |
| gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta | 427 |
| Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu | |
| 55 60 65 70 | |
| ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa | 475 |
| Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu | |
| 75 80 85 | |
| cgg cag ccg cga gac cgc ttc gta cgt cct cac caa cgg ctc ggc acg | 523 |
| Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr | |
| 90 95 100 | |
| ctt cgt cct cac ctc cgt cat caa gcc cgc cac ccc ctg ggg cca ctt | 571 |
| Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu | |
| 105 110 115 | |
| cct cgc cga cca tgt ggc cga gca cgg cga cgg cgt cgt cga cct cgc | 619 |
| Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Pro Arg | |
| 120 125 130 | |
| cat cga ggt ccc gga cgc ccg cgc cgc cca cgc gta cgc gat cga gca | 667 |
| His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala | |
| 135 140 145 150 | |
| cgg cgc ccg ctc ggt cgc cga gcc gta cga gct gaa gga cga gca cgg | 715 |
| Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg | |
| 155 160 165 | |
| cac ggt cgt cct cgc cgc gat cgc cac cta cgg caa gac ccg cca cac | 763 |
| His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His | |
| 170 175 180 | |
| cct cgt cga ccg gac cgg cta cga cgg ccc cta cct ccc cgg cta cgt | 811 |
| Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg | |
| 185 190 195 | |

ggc cgc cgc ccc gat cgt cga acc gcc cgc cca ccg cac ctt cca ggc 859
 Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly
 200 205 210

cat cga cca ctg cgt cgg caa cgt cga gct cgg ccg gat gaa cga atg 907
 His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met
 215 220 225 230

ggt cgg ctt cta caa caa ggt cat ggg ctt cac gaa cat gaa gga gtt 955
 Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Glu Gly Val
 235 240 245

cgt ggg cga cga cat cgc gac cga gta ctc ggc gct gat gtc gaa ggt 1003
 Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly
 250 255 260

cgt ggc cga cgg cac gct caa ggt caa gtt ccc gat caa cga gcc cgc 1051
 Arg Gly Arg Arg His Ala Gln Gly Gln Val Pro Asp Gln Arg Ala Arg
 265 270 275

cct cgc caa gaa gaa gtc cca gat cga cga gta cct gga gtt cta cgg 1099
 Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg
 280 285 290

cgg cgc ggg cgt cca gca cat cgc gct gaa cac ggg tga catcgtcgag 1148
 Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly
 295 300 305

acggtacgca cgatgcgcgc cgccggcgctc cagttcctgg acacgcccgca ctcgtactac 1208
 gagaccctcg gggagtgggt gggcgacacc cgcgtccccg tcgacaccct gcgcgagctg 1268
 aagatcctcg cggaccgca cgaggacggc tatctgctcc agatcttcac caagccggtc 1328
 caggaccgcc cgacggtctt cttcgagatc atcgaacgcc acggctcgat gggattcggc 1388
 aagggcaact tcaaggccct gttcgaggcg atcgagcggg agcaggagaa gcggggcaac 1448
 ctgtaggcgg cgcggcccgg g 1469

<210> 6
 <211> 306
 <212> PRT
 <213> *Streptomyces avermitilis*
 <400> 6
 Met Gln Pro His Ala Met Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly

17

260

265

270

Pro Asp Gln Arg Ala Arg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg
 275 280 285

Val Pro Gly Val Leu Arg Arg Arg Gly Arg Pro Ala His Arg Ala Glu
 290 295 300

His Gly
 305

<210> 7

<211> 1479

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1401)

<400> 7

atg gcg acg acg gtt aca ctc aaa tcc ttc acc gga ctt cgt caa tca 48
 Met Ala Thr Thr Val Thr Leu Lys Ser Phe Thr Gly Leu Arg Gln Ser
 1 5 10 15

tca acg gag caa aca aac ttc gtc tct cat gta ccg tca tca ctt tct 96
 Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser
 20 25 30

ctc cct caa cga cgg acc tct ctc cga gta acc gca gcc agg gcc act 144
 Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr
 35 40 45

ccc aaa ctc tcc aac cgt aaa ctc cgt gtc gcc gtc atc ggt ggt gga 192
 Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly
 50 55 60

cca gca ggc ggg gca gct gca gag act cta gca caa gga gga atc gag 240
 Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu
 65 70 75 80

acg att ctc atc gag cgt aag atg gac aat tgc aag cct tgc ggt ggc 288
 Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly
 85 90 95

gcg att cct ctc tgt atg gtc gga gaa ttc aac ttg ccg ttg gat att 336
 Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile

| 100 | 105 | 110 | |
|-----------------------------------------------------------------|-----|-----|-----|
| att gat cgg aga gtg acg aag atg aag atg att tcg ccg tcg aac att | | | 384 |
| Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile | | | |
| 115 | 120 | 125 | |
| gct gtt gat att ggt cgt acg ctt aag gag cat gag tat ata ggt atg | | | 432 |
| Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met | | | |
| 130 | 135 | 140 | |
| gtg aga aga gaa gtt ctt gat gct tat ctg aga gag aga gct gag aag | | | 480 |
| Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys | | | |
| 145 | 150 | 155 | 160 |
| agt gga gcc act gtg att aac ggt ctc ttc ctt aag atg gat cat ccg | | | 528 |
| Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro | | | |
| | 165 | 170 | 175 |
| gag aat tgg gac tcg ccg tac act ttg cat tac act gag tac gat ggt | | | 576 |
| Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly | | | |
| | 180 | 185 | 190 |
| aaa act gga gct aca ggg acg aag aaa aca atg gag gtt gat gct gtc | | | 624 |
| Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val | | | |
| 195 | 200 | 205 | |
| att gga gct gat gga gct aac tct agg gtt gct aaa tct att gat gct | | | 672 |
| Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala | | | |
| 210 | 215 | 220 | |
| ggt gat tac gac tac gca att gca ttt cag gag agg att agg att cct | | | 720 |
| Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro | | | |
| 225 | 230 | 235 | 240 |
| gat gag aaa atg act tac tat gag gat tta gct gag atg tat gtt gga | | | 768 |
| Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly | | | |
| | 245 | 250 | 255 |
| gat gat gtg tcg ccg gat ttc tat ggt tgg gtg ttc cct aag tgc gac | | | 816 |
| Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp | | | |
| 260 | 265 | 270 | |
| cat gta gct gtt gga aca ggt act gtg act cac aaa ggt gac atc aag | | | 864 |
| His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys | | | |
| 275 | 280 | 285 | |
| aag ttc cag ctc gcg acc aga aac aga gct aag gac aag att ctt gga | | | 912 |
| Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly | | | |

| | | | |
|-----------------------------------------------------------------|-----|-----|------|
| 290 | 295 | 300 | |
| ggg aag atc atc cgt gtg gag gct cat ccg att cct gaa cat ccg aga | | | 960 |
| Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg | | | |
| 305 | 310 | 315 | 320 |
| cca cgt agg ctc tcg aaa cgt gtg gct ctt gta ggt gat gct gca ggg | | | 1008 |
| Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly | | | |
| 325 | 330 | | 335 |
| tat gtg act aaa tgc tct ggt gaa ggg atc tac ttt gct gct aag agt | | | 1056 |
| Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser | | | |
| 340 | 345 | | 350 |
| gga aga atg tgt gct gaa gcc att gtc gaa ggt tca cag aat ggt aag | | | 1104 |
| Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys | | | |
| 355 | 360 | | 365 |
| aag atg att gac gaa ggg gac ttg agg aag tac ttg gag aaa tgg gat | | | 1152 |
| Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp | | | |
| 370 | 375 | | 380 |
| aag aca tac ttg cct acc tac agg gta ctt gat gtg ttg cag aaa gtg | | | 1200 |
| Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val | | | |
| 385 | 390 | | 400 |
| ttt tac aga tca aat ccg gct aga gaa gcg ttt gtg gag atg tgt aat | | | 1248 |
| Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn | | | |
| 405 | 410 | | 415 |
| gat gag tat gtt cag aag atg aca ttc gat agc tat ctg tac aag cgg | | | 1296 |
| Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg | | | |
| 420 | 425 | | 430 |
| gtt gcg ccg ggt agt cct ttg gag gat atc aag ttg gct gtg aac acc | | | 1344 |
| Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr | | | |
| 435 | 440 | | 445 |
| att gga agt ttg gtt agg gct aat gct cta agg aga gag att gag aag | | | 1392 |
| Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys | | | |
| 450 | 455 | | 460 |
| ctt agt gtt taagaaacaa ataatgaggt ctatctcctt tcttcatctc | | | 1441 |
| Leu Ser Val | | | |
| 465 | | | |
| tatctctcctt tttttgtctg ttagtaatct atctacac | | | 1479 |

<210> 8

<211> 467

<212> PRT

<213> Arabidopsis thaliana

<400> 8

Met Ala Thr Thr Val Thr Leu Lys Ser Phe Thr Gly Leu Arg Gln Ser
 1 5 10 15

Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser
 20 25 30

Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr
 35 40 45

Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly
 50 55 60

Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu
 65 70 75 80

Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly
 85 90 95

Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile
 100 105 110

Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile
 115 120 125

Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met
 130 135 140

Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys
 145 150 155 160

Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro
 165 170 175

Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly
 180 185 190

Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val
 195 200 205

Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala
 210 215 220

Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro
 225 230 235 240

Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly
 245 250 255

Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp
 260 265 270

His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys
 275 280 285

Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly
 290 295 300

Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg
 305 310 315 320

Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly
 325 330 335

Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser
 340 345 350

Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys
 355 360 365

Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp
 370 375 380

Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val
 385 390 395 400

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn
 405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg
 420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr
 435 440 445

Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys
 450 455 460

Leu Ser Val
 465